

[illegible]

FIG. 1A

[illegible]

FIG. 2A

[illegible]

FIG. 2B

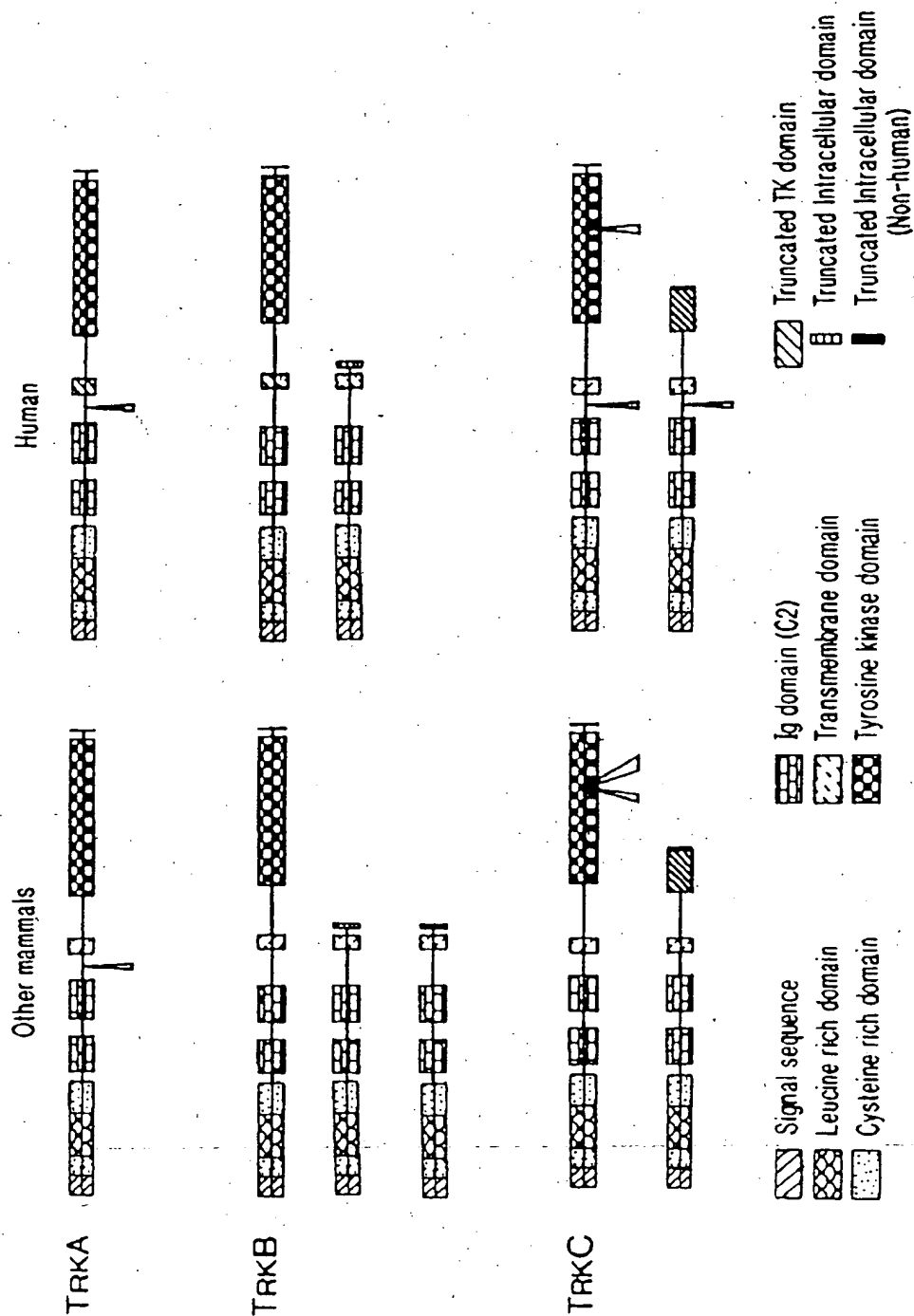


FIG. 4

62

[illegible]

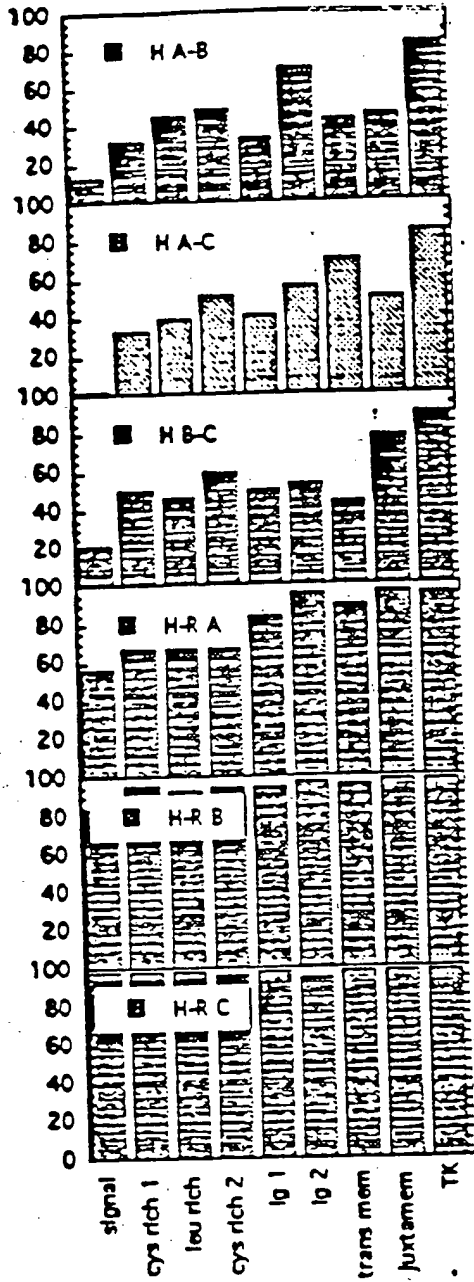


1590 TGGGCTCTTTCAAAACAGAGACATCATGGGATATTAAACTTCAAGGACATAGAGATCATCTAGTCCGATCACTACTATATATATAGCAAGACCTGAGGTCACAGCTGGGCAAGTGTCT
498 M V F S M I D M H G I L N L E D M R D E L V P S T N T Y I Y E E P E V Q S G E V S

2710 TACTCAAGGTCACATGGTTTCAGAGAAATTATGTTCAATCGATAGAGCTTCCGAGCACTTCAAGCTCTTAAGCATGCGCATCTATGTTGAGCATGTCGATGTTTATTTCAAGCAAGGA
538 Y P R S H G C F R E I M L N P I S L P G N S E P L N H G I Y V E D V M V Y F S R C

1830 GGTCAATGCTTTTAAAAAC
578 R H G F O

Figure 3



Figur 4

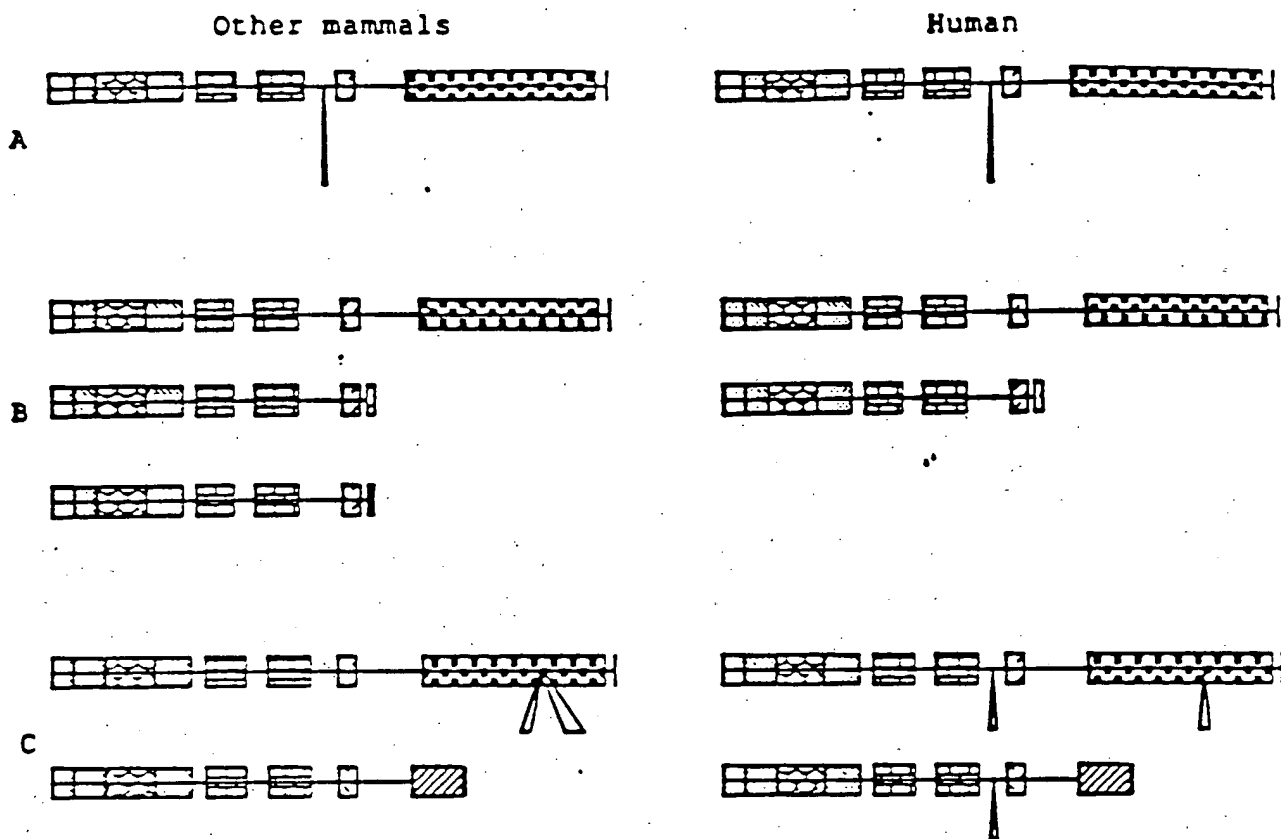


Figure 5

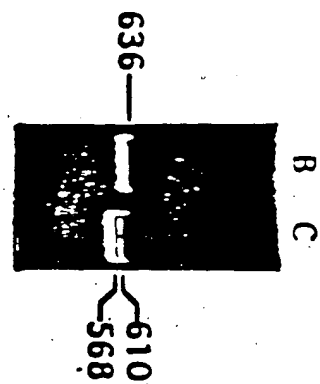


Figure 6

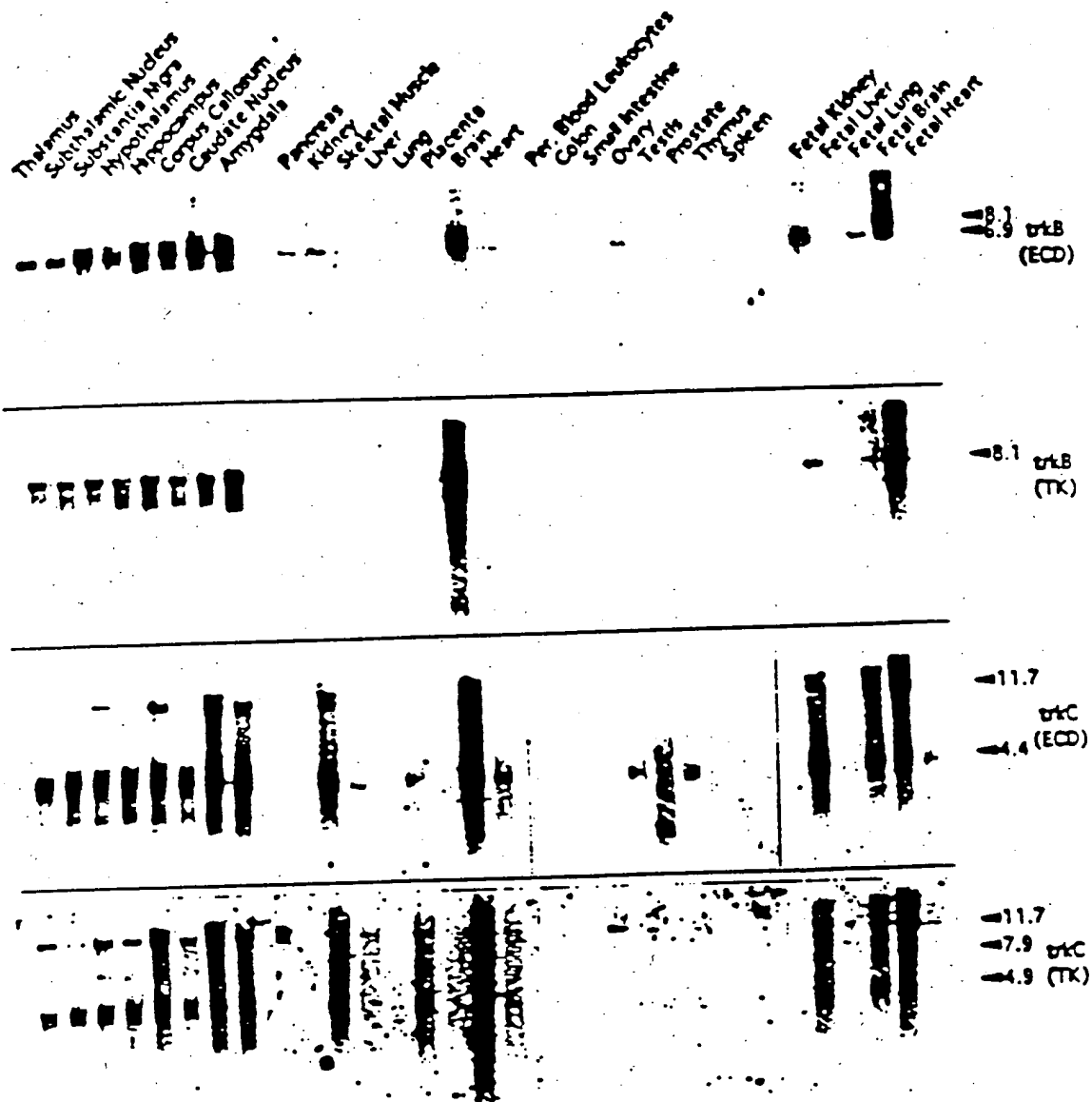
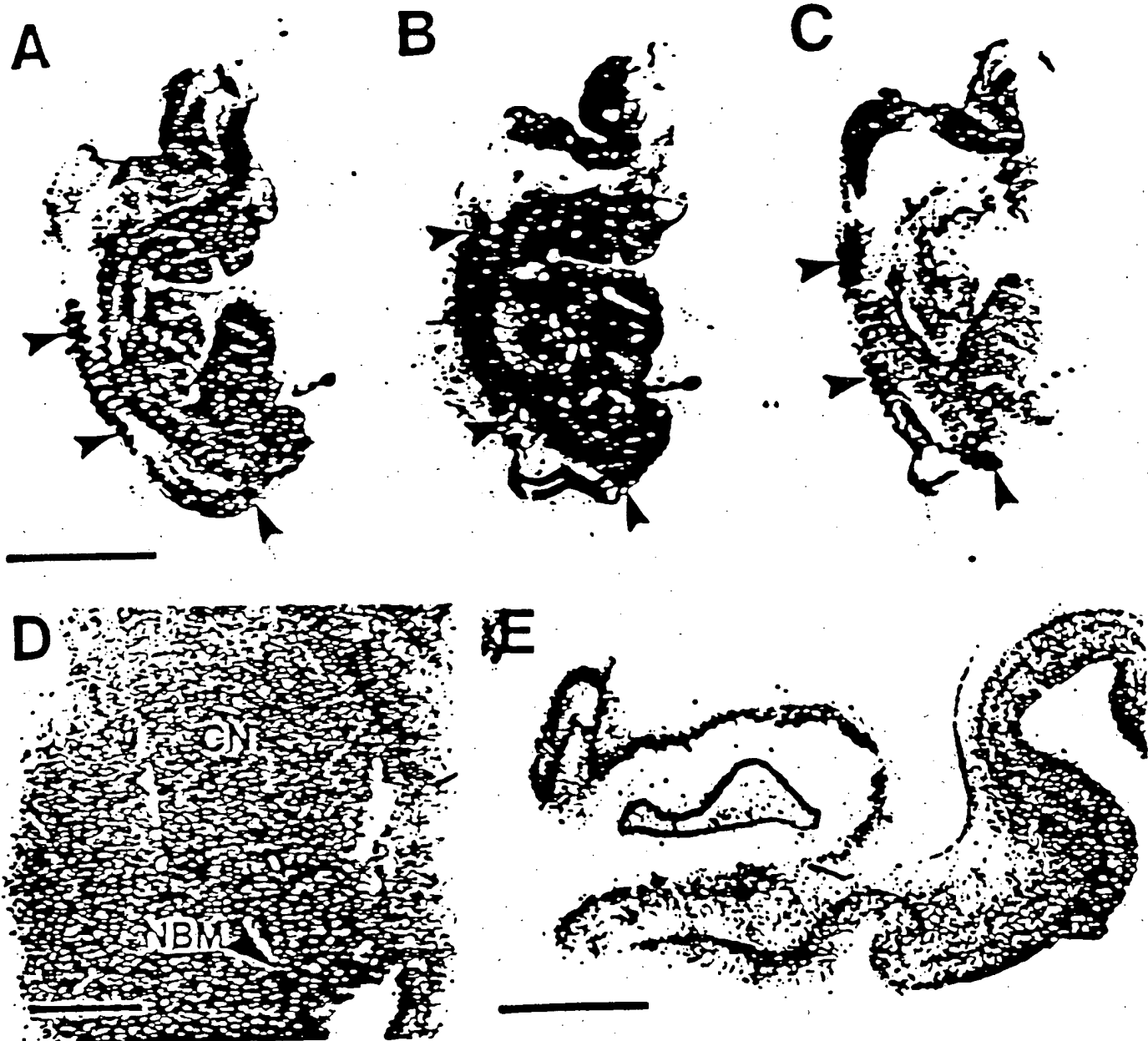


Figure 7



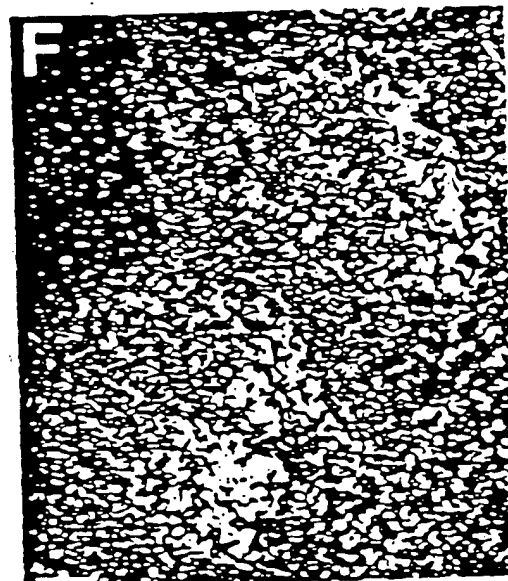
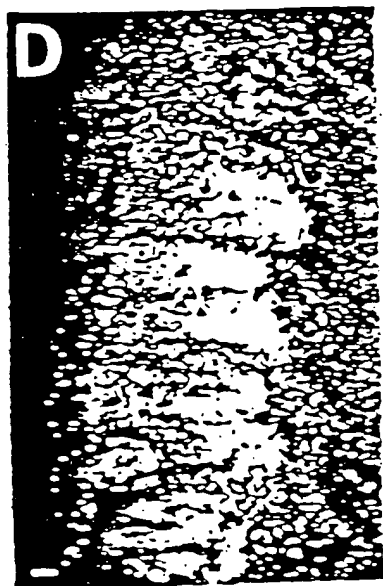
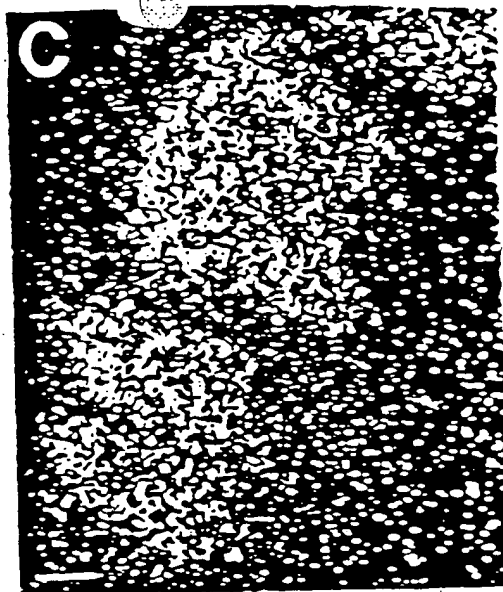
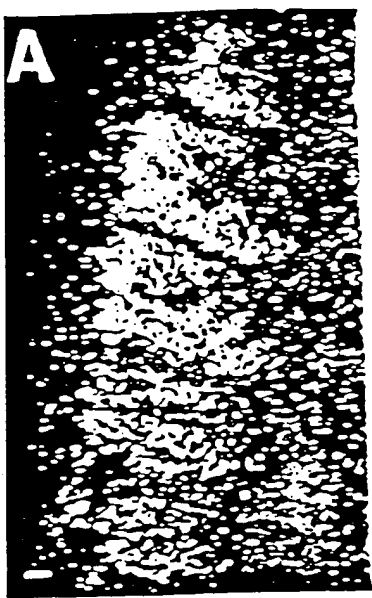


Figure 8

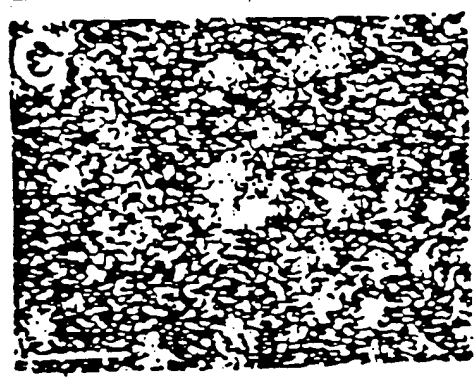
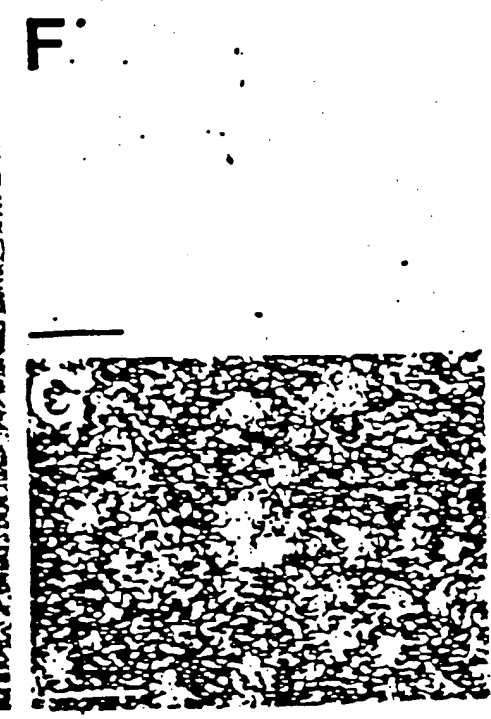
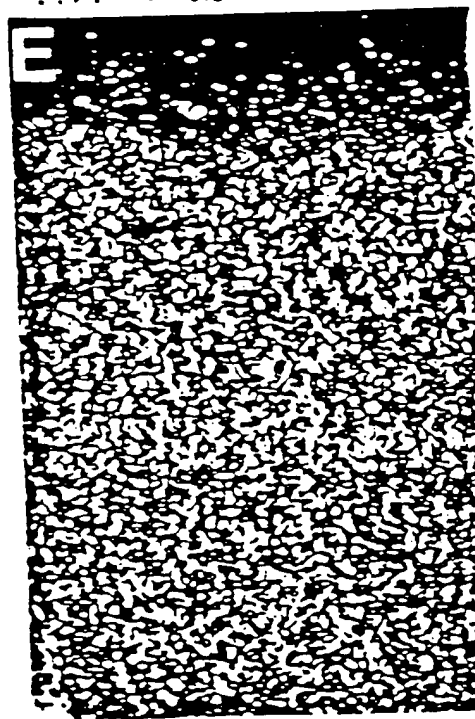
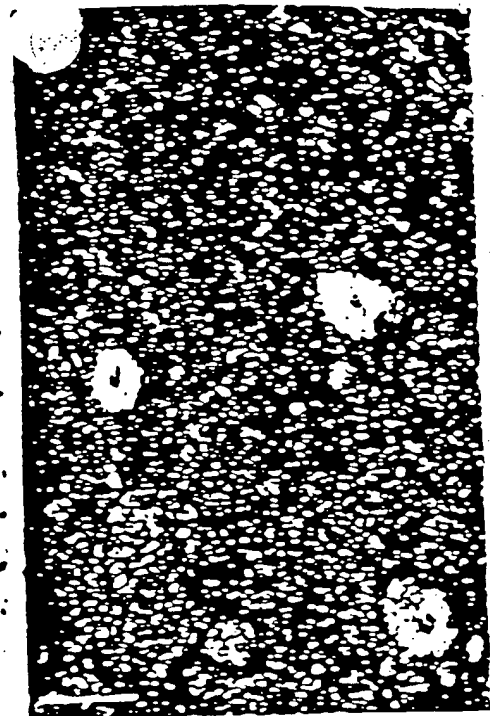
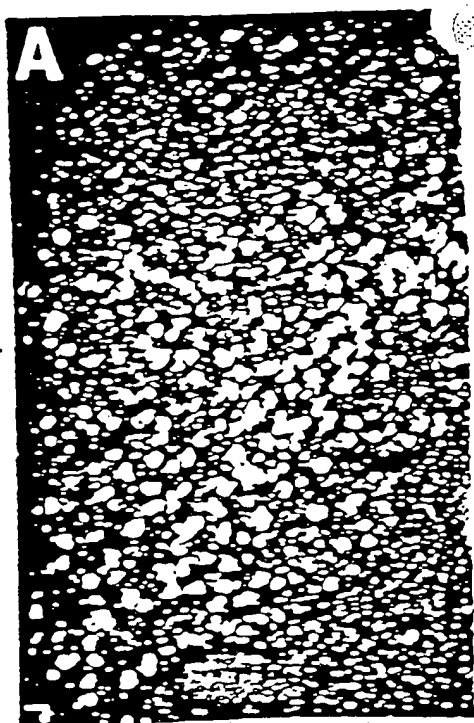


Figure 9

Figure 10

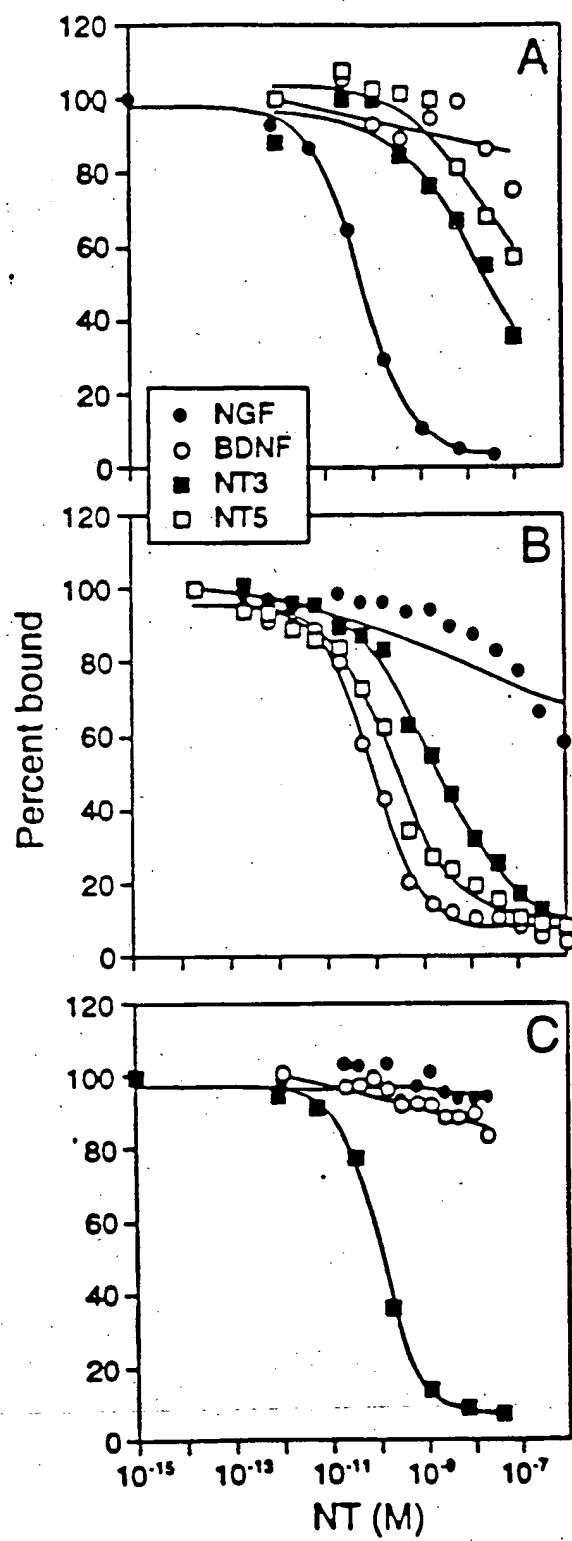


Figure 11

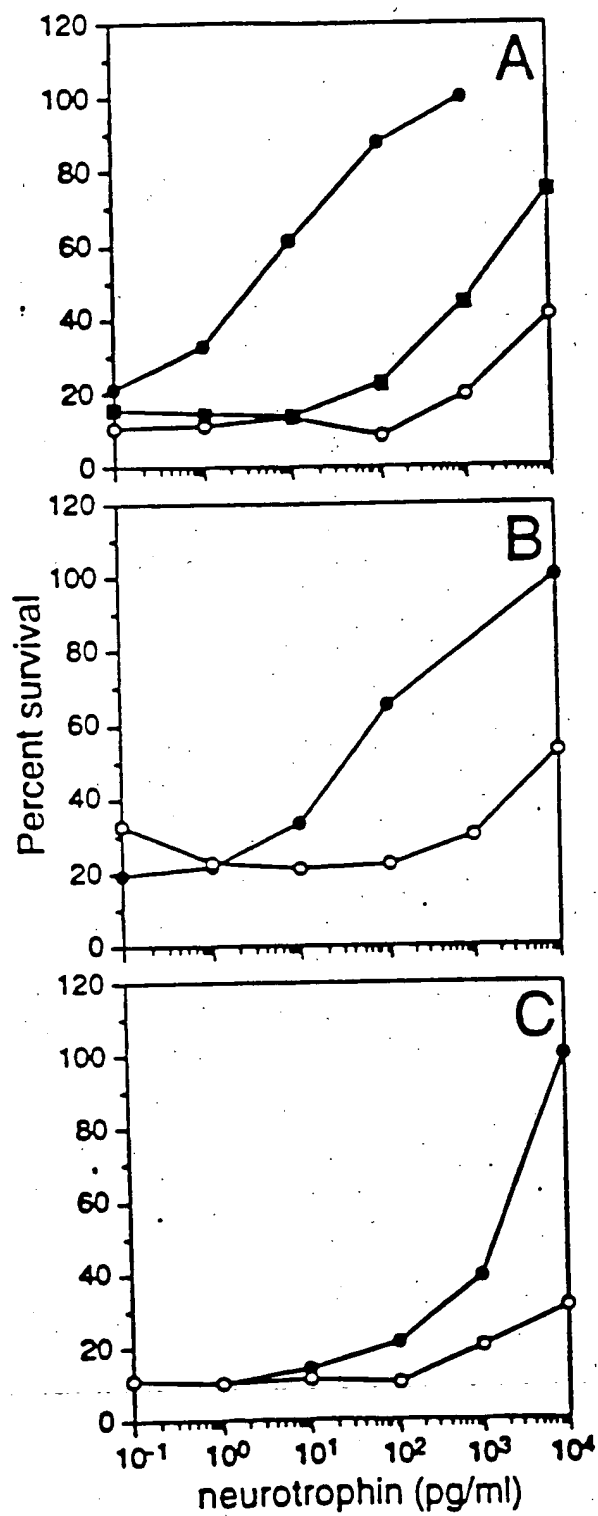


Figure 12

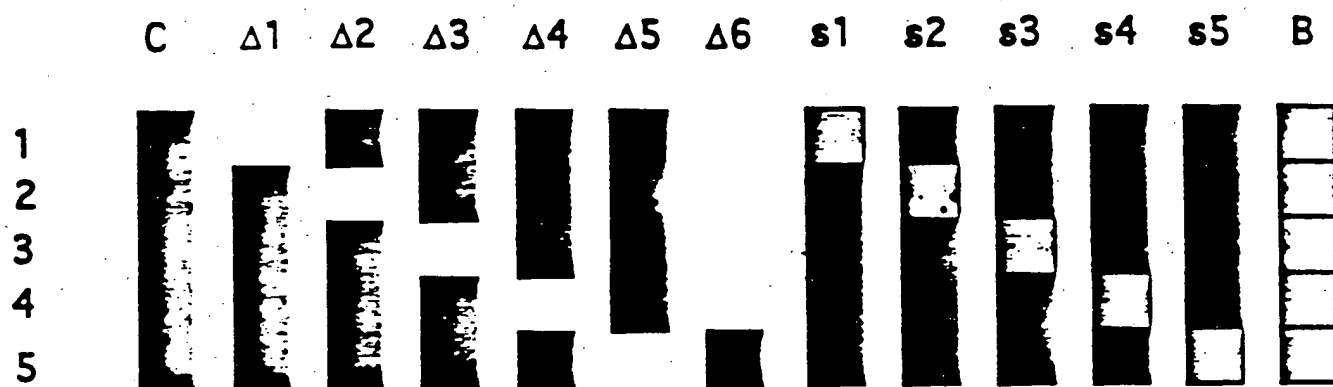


Figure 13

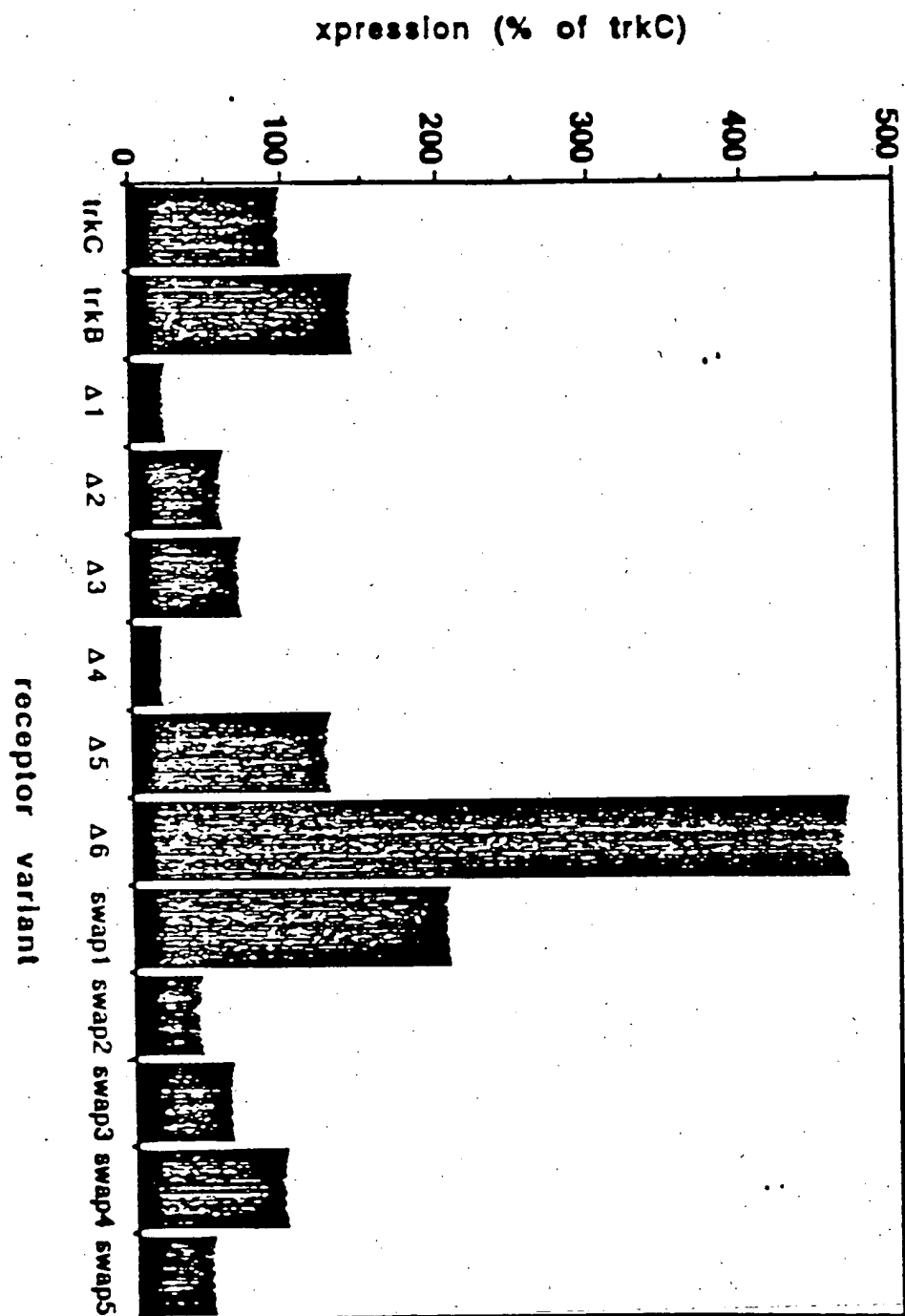


Figure 14A

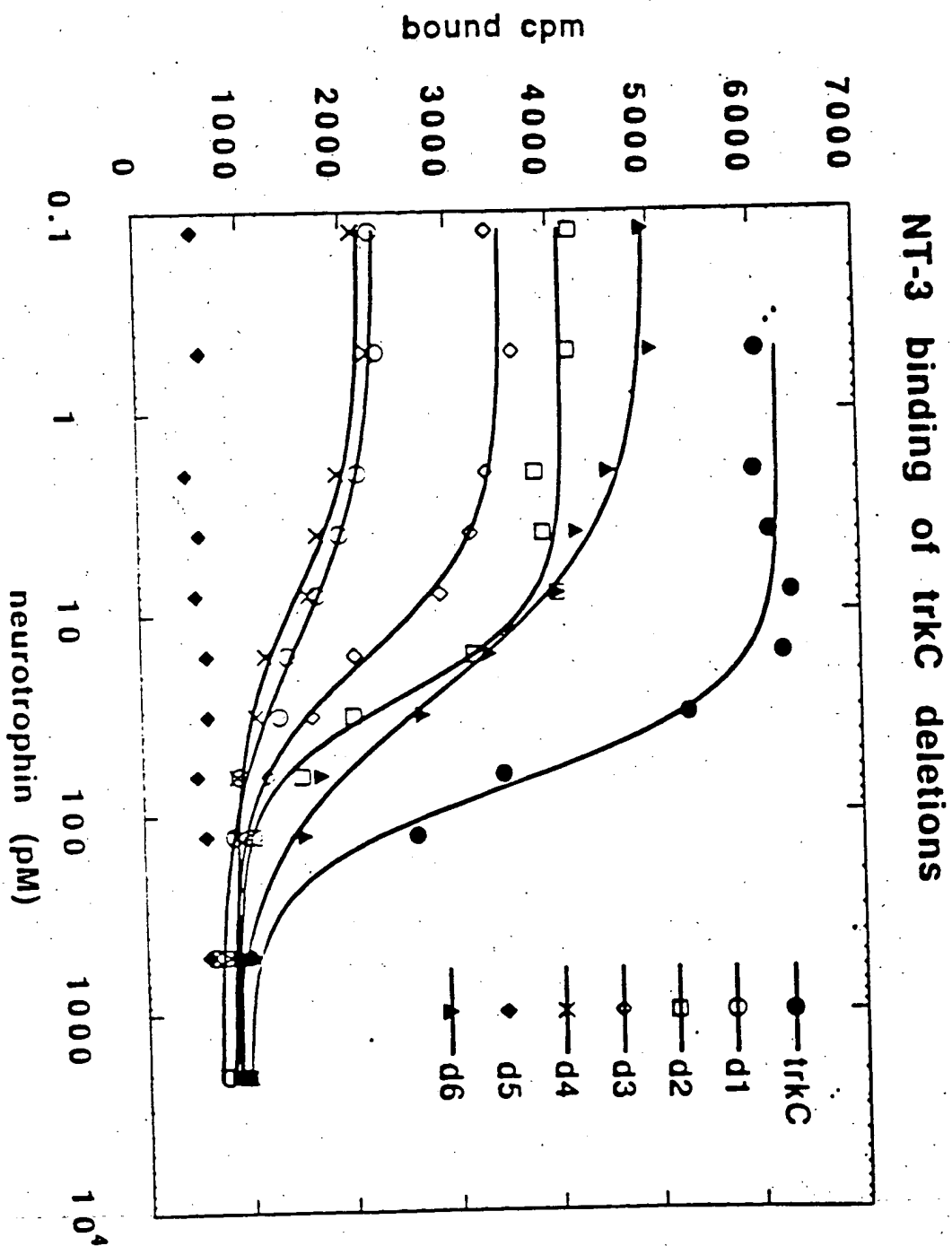


Figure 14B

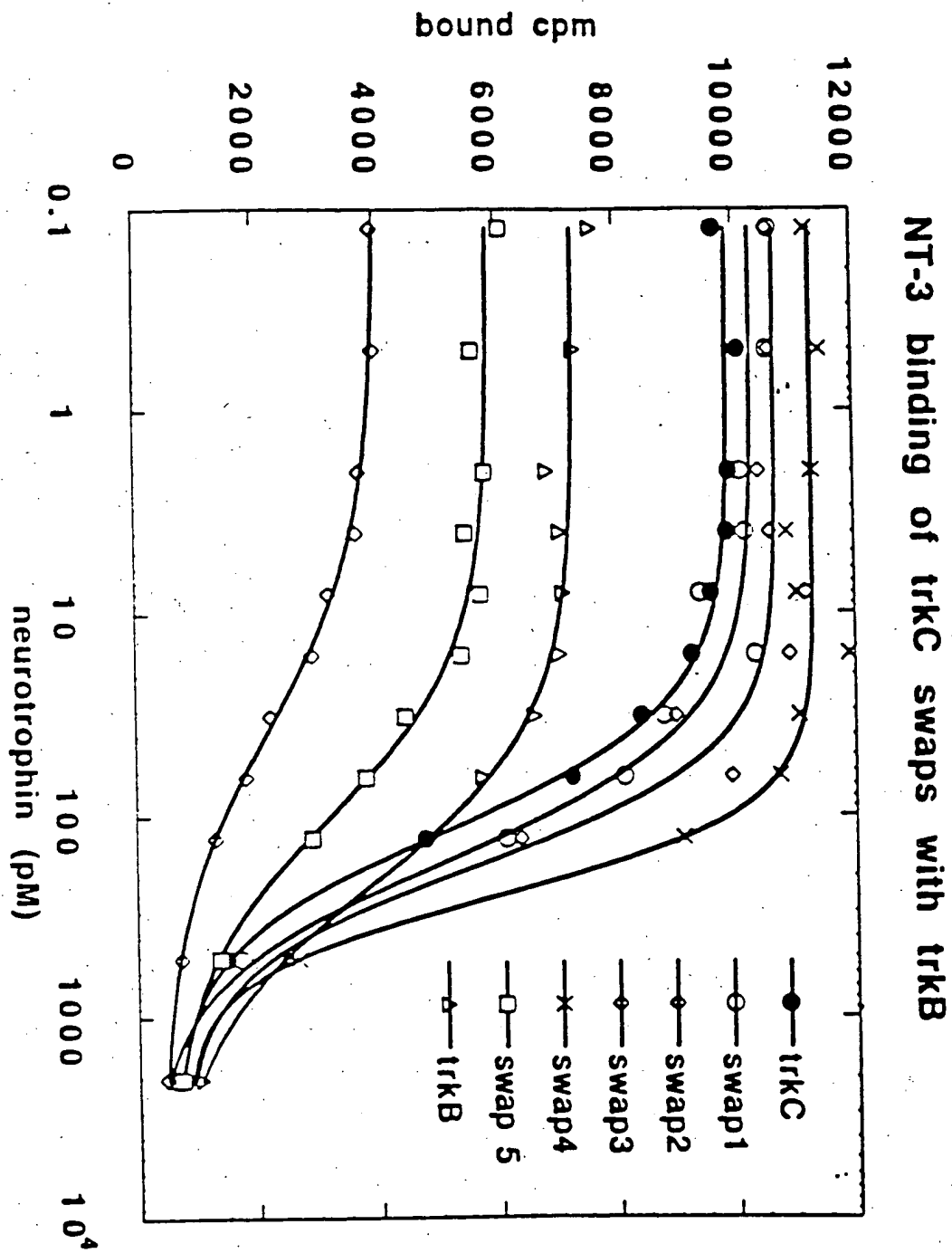
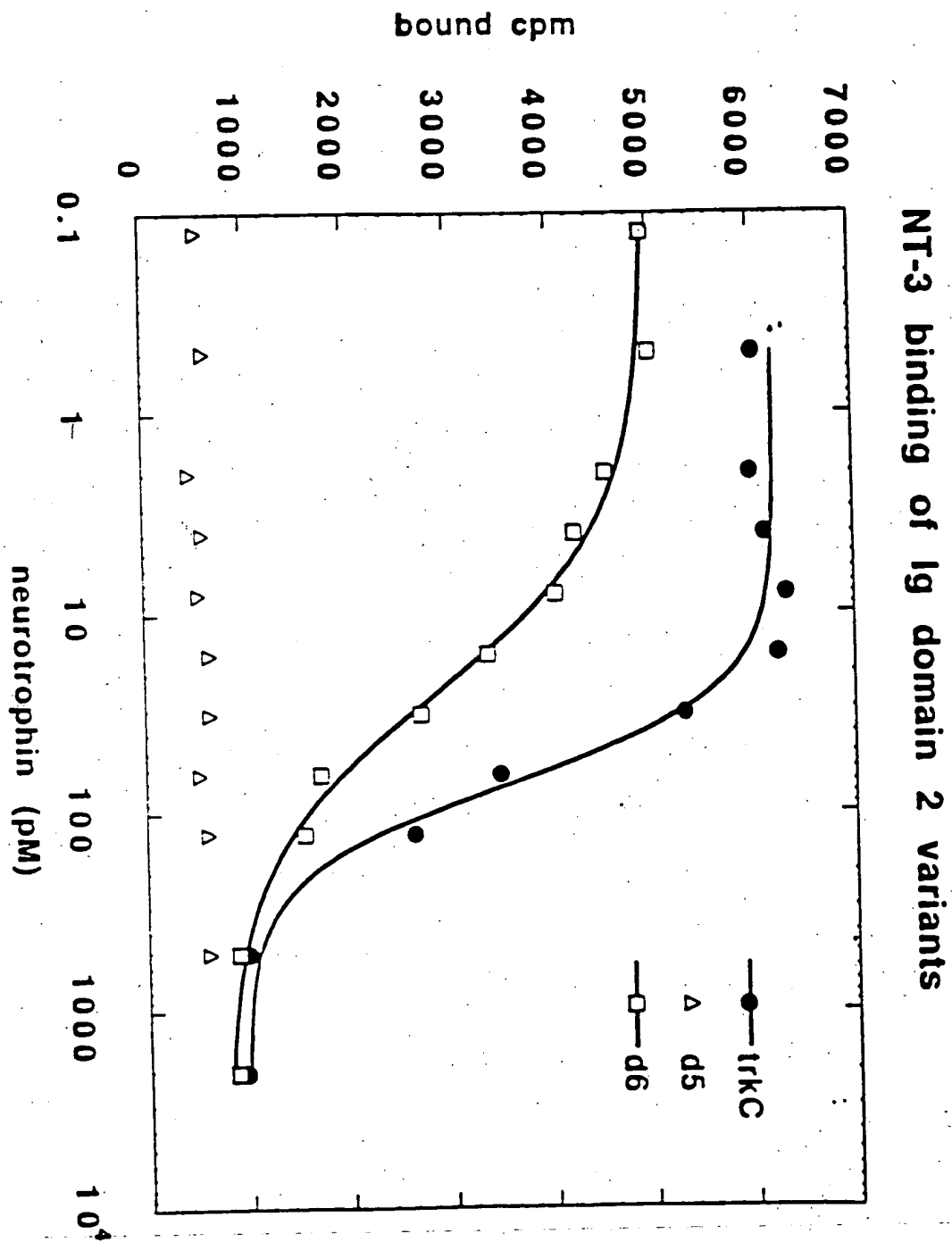
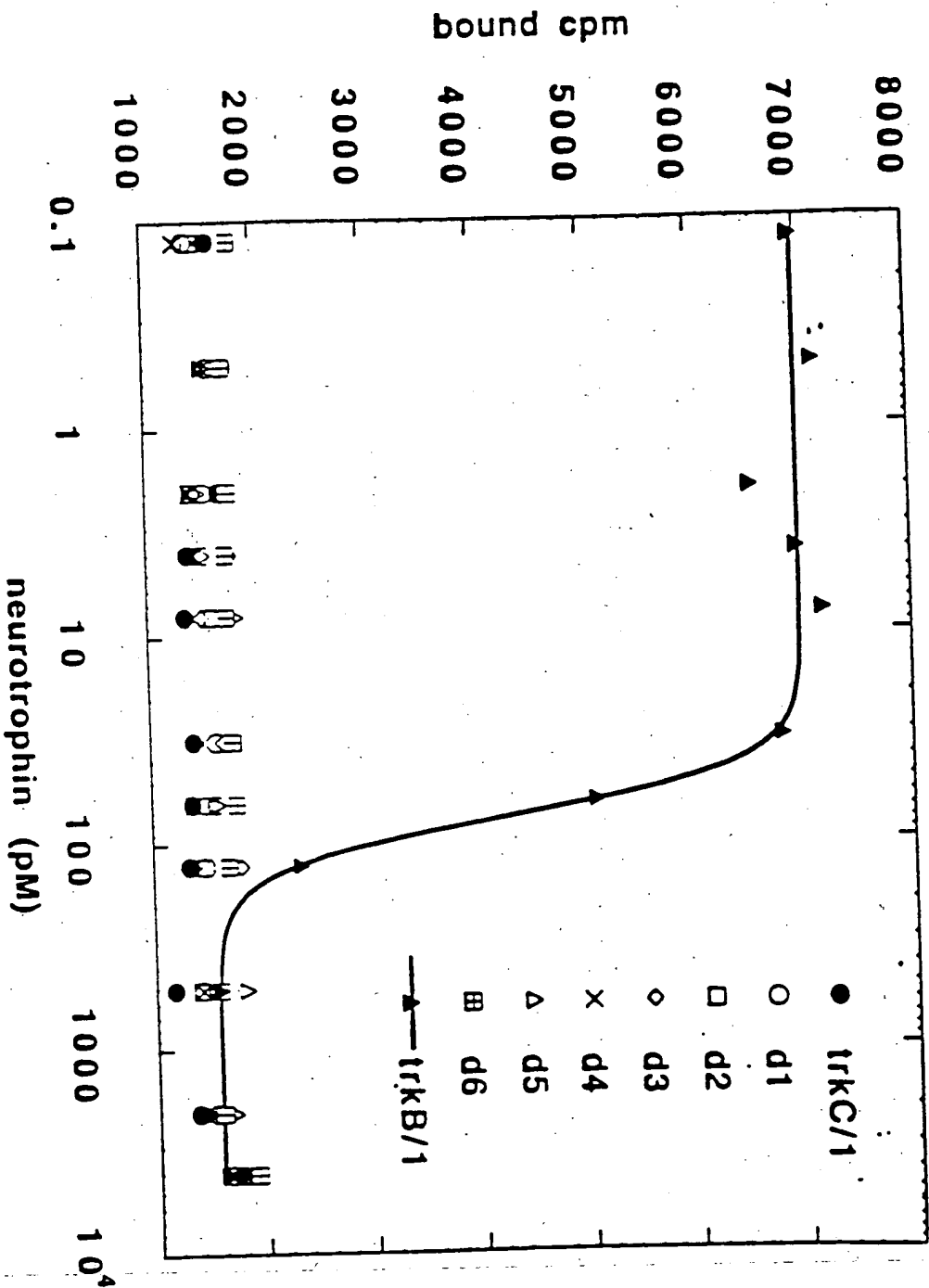


Figure 14C



BDNF binding of deletions of trkB



BDNF binding of trkB swaps with trkB

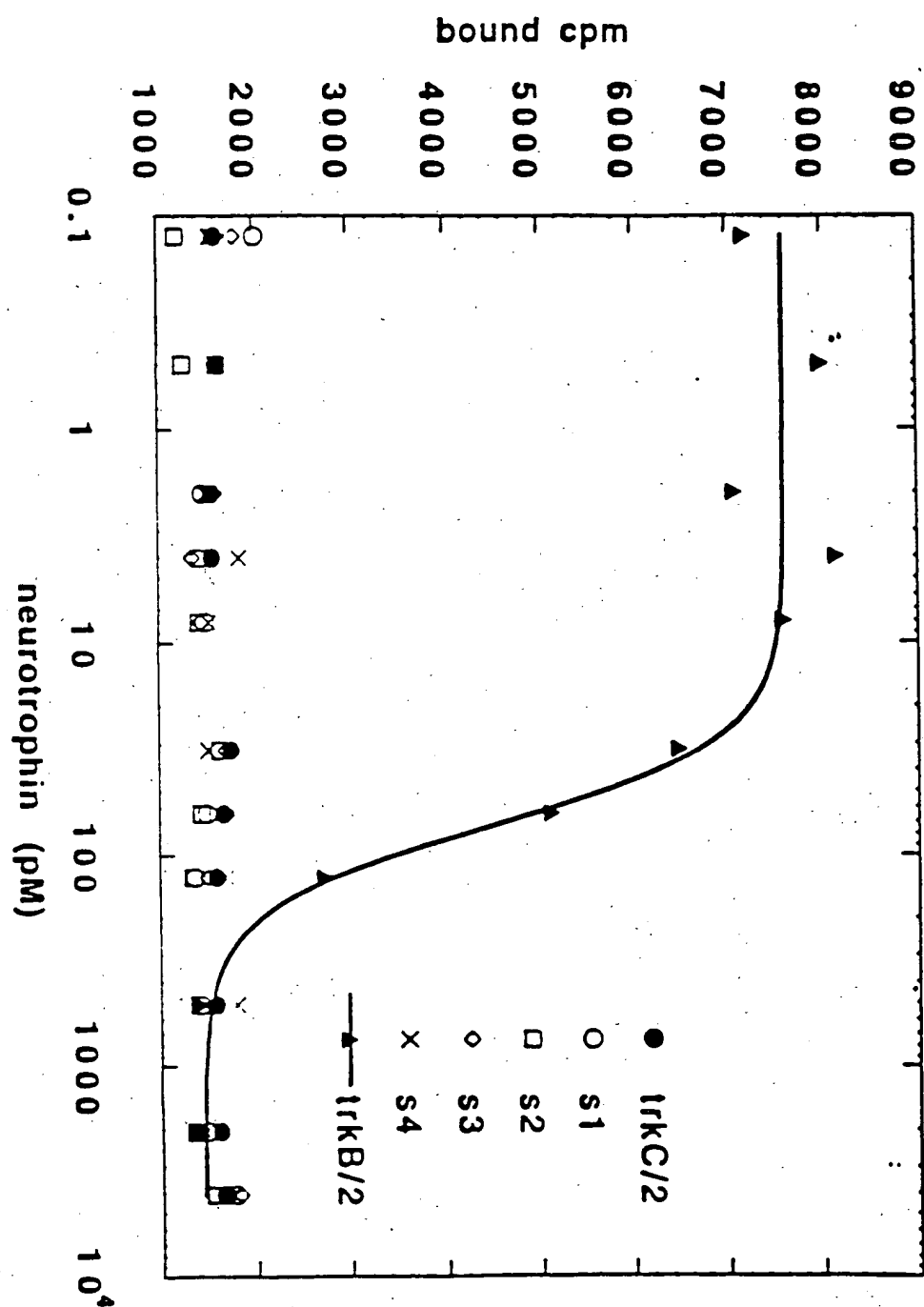
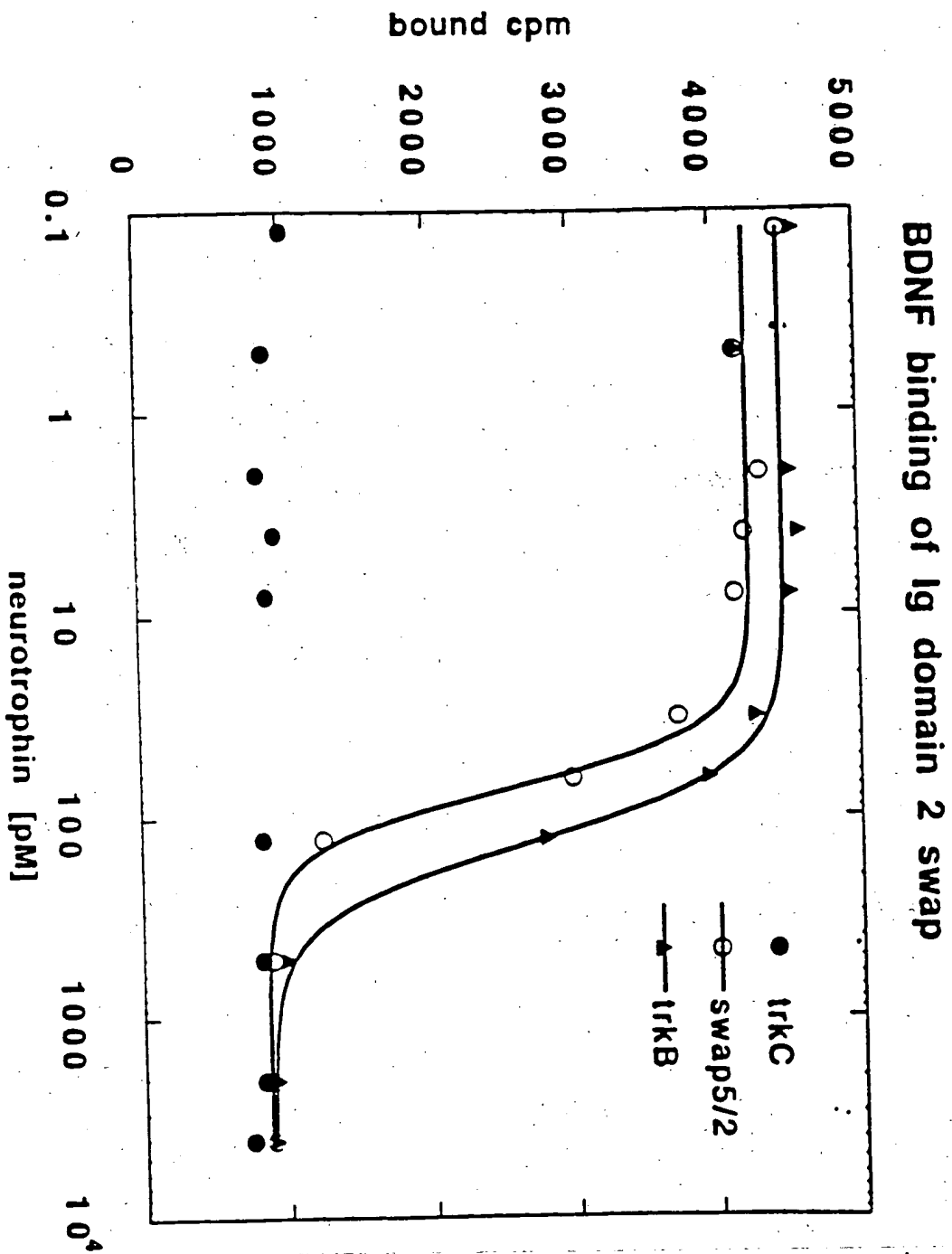


Figure 15C




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/-----Signal-----/-----Cysteine Rich 1-----/
trkA 1 MLRGGRGQLGWSWAGPGSLLAWLILAS-----AGAAACPDACCPHGSSGLRCTR-DGALDSLHMLPG-----AENITELYIENOO
trkB 1 HSSWIRWHGPMARLWGFQNLVVGFW-----RAAFACPTS-CKCSASRIWCSDPSPGIVAFPRLEPNSVD-----PENITEIFIANOK
trkC 1 HDVSL-----CPAKCSFWRI-FLGCSVWLDYVGSVLA-PAN-CVCSKTEINCRAPDDGNL-FPLLEGQDSQSNCHNANINITDISRMTSINIEWR

/-----Leucine Rich-----/-----Cysteine
trkA 78 HLQHELRDLRGLGELRNLTIVKSGLRFPVAPDAFHFTPLRSRLNLSFNALESLSWKTVQGLSLOELVLSGNPLWCSCLARMLQRWEEGLGCVPEOKLOC
trkB 78 RLEIINEDDVEAYVGLRNLTIVDSGLKFVANKAFKKNLNQHNIFTRNKLTSLSRKHFRHLDSELIIVGNPPTCSDIMNKTLOE-AKSSPDQDLYC
trkC 90 SLHTLNADVMEHYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTTLWQLFOTLSRELOLEQWFFNCSCDIRNMQLMOEGEAKLNSQNLVC

/-----Rich II-----/-----Immunoglobulin I-----/
trkA 178 HGQG-----PLAMPHASCCVPTLKVQVFNASVDVGDVLLRQVQEGRLQAGNLTLEQSATVMKS-----GGLPSLGLTLANVTSDLRNKNLTCAEN
trkB 177 LNESSKNIPLANIQIPNCCPSANLAAPNLTVEEGKSLTSCSVAGDPVFNHYWQGNLVSKHNNET-----SHTQG-SLRITNISDDSGKQISCVAEHL
trkC 190 INADGSQLPLFRHNSIQCDLPEISVSHVNLTVREGDNNAVITCNGSGSLPDVDNIVTGLQSIINTQTNLWTVHAINLTLVNVTSEDNGFTLTICIAENV

/-----Immunoglobulin II-----/
trkA 271 VGRAEVSQVNVVSPASVO-LHTAVEMHH-CIPFSVDGQPAPSLRWLFNGSVLNETSFITFELEPAANETVRHGCLRLNQPTVMNNGNYTLAANPFQO
trkB 272 VGEDQDSVNLTVHFAPTITFLSPTSDMH-CIPFTVKGNPKPALOWFYNGAILNESKYICTKIN--VTNHTIYHGCGLQDNPTMNNNGDYTLIAKNEYK
trkC 290 VQMSNASVALTVYPPRVVSLEPELRLE-CIEFVVRGNPPPTLHWLWNGQPLRESKIHVEY--QGEIS-EGCLLFNKPPTMNNNGNYTLIAKNEP LGT

/-----Transmembrane-----/
trkA 370 ASASIMAAFH-----DNPF-----EF-NPEDPIPDTS-----TSGDPVEKKDET-----FGVSVAVGLAVFACLFSLTLLVINKCGRNKKFGIN
trkB 370 DEKQISAHFMGWP GIDGAPNYPDVYIYEDYCTAANDIGDTNRSNEIPSTDVDTKTGREHLSVAVVVIASVVGFC-LLVHLFLL-KLARHSKFGHK
trkC 387 ANQTINGHFL-----KEPFEST-DNF-ILFDEVSPT-----PPIVTVTHKPEED-----FGVSIAGVLAATACVLLVVLVFMH-KYGRRSKFGHK

/-----Juxtamembrane-----/
trkA 446 RP-AVLAPEDGLAMSLHMTLGGSSLSPT-CKGSGLOG-----HIIENPOYF-----SDACVHHIKRDIVLKWLGEAGFGKVFLAECNHLPEQD
trkB 466 GPASVISNDDDSASPLHHISNGSNTPSSSEGGPDVITGHTKIPVIENPOYFGITNSQLKPDITVQHIKRNIVLKLRELGEAGFGKVFLAECYNLCPEQD
trkC 466 GPVAVISGEEDSASPLHHINHGITTTPSSLDAGPDTVIGHTRIPIVNIENPOYFROGMNCHKPDTTVQHIKRDIVLKLRELGEAGFGKVFLAECYNLSPTKD

/-----Tyrosine Kinase-----/
trkA 532 KMLVAVKALKEASESARQDFQREAEILLTLQHQHIVRFFGVCTEGRPLLHVFEYMRHGDINRFLRSHGPDAKLLAGGEDV-APGFLGLGQLLAVASQVAA
trkB 566 KILVAVKTLKQASDNARKQFHREAEILLTLQHEHIVKFGVCGVEGDLIMVFEYMKHGDINRFLRSHGPDVILMAEGNPP-----TELTSQMLHIAQOIAA
trkC 566 KMLVAVKALKOPTLAARKQFQREAEILLTLQHEHIVKFGVCGGQDPLIMVFEYMKHGDINRFLRSHGPDAMI LVDGQPRQAKGELGLSOMLHIASQIAS

/-----/
trkA 631 GMVYLASQHFVHRDLATRNCLVGGGLVVKIGDFGMSRDVYSTDYRVGGHTMLPIRWMPPEISILYRKFTTESDVWSFGVVLWEIFTYKQPNYQLSNTEA
trkB 663 GMVYLASQHFVHRDLATRNCLVGENLVKIGDFGMSRDVYSTDYRVGGHTMLPIRWMPPEISIMYRKFTTESDVWSLGVVLWEIFTYKQPNYQLSNNEV
trkC 666 GMVYLASQHFVHRDLATRNCLVGANLVKIGDFGMSRDVYSTDYRVGGHTMLPIRWMPPEISIMYRKFTTESDVWSFGVVLWEIFTYKQPNYQLSNTEV

/-----/
trkA 731 IDGITQGRELERPRACPPPEVYAIMRGCGWQREPQORHSIKDVHARLOALACAPPVYLDVLC
trkB 763 IECITQGRVLRAPRTPQPEVYELMLGCGWQREPQORHAKNIKSHILLONLAKASPVYLDILG
trkC 782 IECITQGRVLRPRVCFKEVYDVMLGCGWQREPQORLNKEIKILHARLOALATPPIYLDILG

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Figure 16

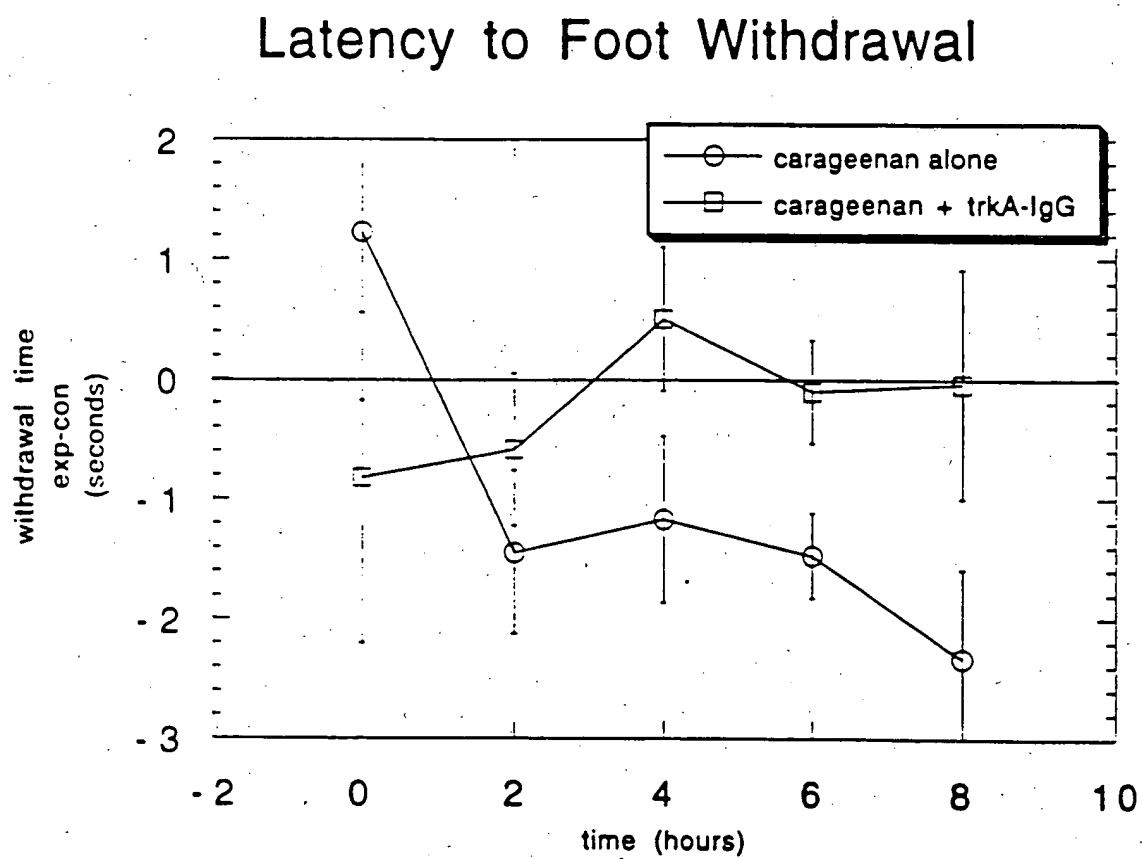


Figure 17

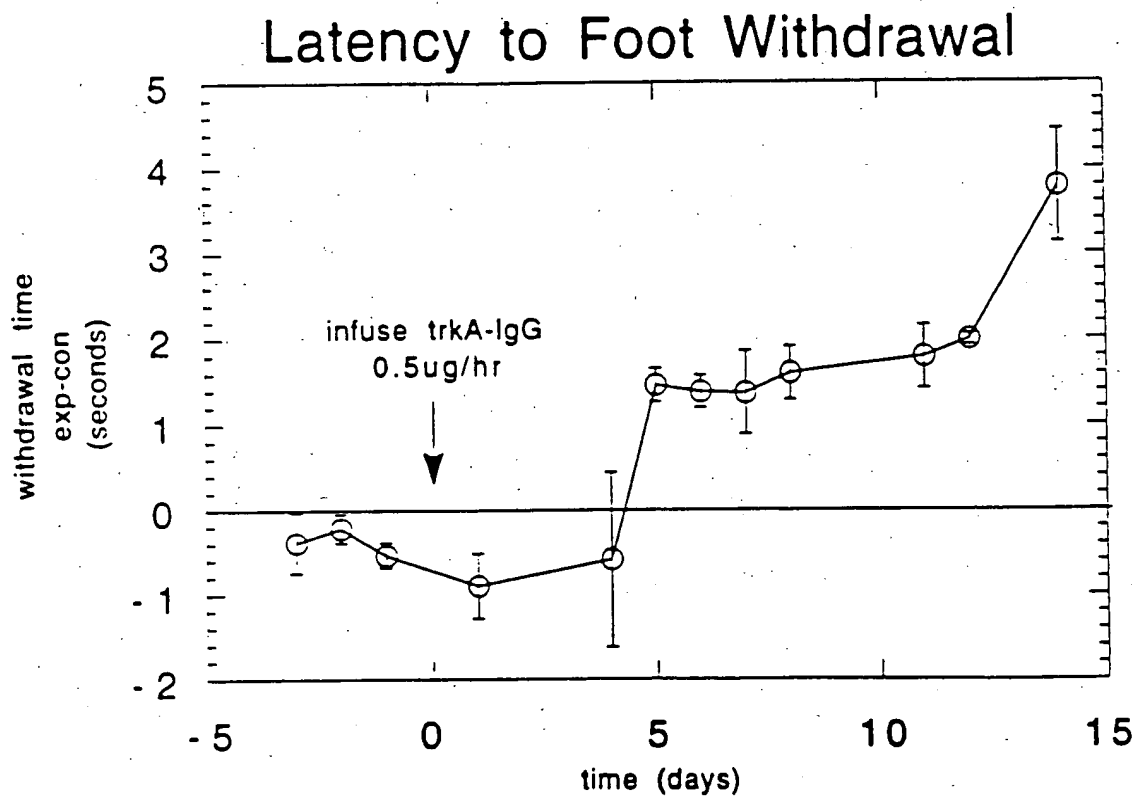


Figure 18